



Blast 2 Sequences results

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Taxonomy

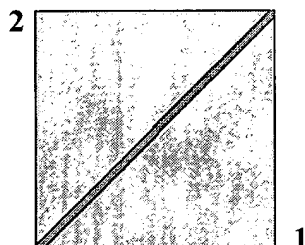
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ Align

Sequence 1 gi 6746554 10-deacetylbaccatin III-10-O-acetyl transferase [Taxus cuspidata] **Length 440 (1 .. 440)**

Sequence 2 gi 18034655 10-deacetylbaccatin III-10-O-acetyl transferase [Taxus baccata] **Length 440 (1 .. 440)**



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 857 bits (2215), Expect = 0.0
 Identities = 430/440 (97%), Positives = 432/440 (97%)

```

Query: 1  MAGSTEFVVRSLERVMVAPSQSPKAFQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP 60
          MAGSTE VVRSLERVMVAPSQSPKAFQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP
Sbjct: 1  MAGSTESVVRSLERVMVAPSQSPKAFQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP 60

Query: 61 AKVIRQALS KVLVYYSPFAGRLRKKENG DLEVECTGEGALFVEAMADTDLSVLGDLDDYS 120
          AKVIRQALS KVLVYYSPFAGRLRKKENG DLEVECTGEGALFVEAMADTDLSVLGDLDDYS
Sbjct: 61 AKVIRQALS KVLVYYSPFAGRLRKKENG DLEVECTGEGALFVEAMADTDLSVLGDLDDYS 120

Query: 121 PSLEQLLFCLPPD TDIEDIHPLVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM 180
          PSLEQLLFCLPPD TDIEDIHPLVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM
Sbjct: 121 PSLEQLLFCLPPD TDIEDIHPLVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM 180

Query: 181 ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHFQLICPPSTFGKIVQGSLVITSETINCIK 240
          ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHF+LI PPSTFGKIVQGSL ITSETI IK
Sbjct: 181 ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHFRLIRPPSTFGKIVQGSLGITSETIKWIK 240

Query: 241 QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMDMRKLFNPPLSKGYGN 300
          QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMDMRKLFNPPL KGYGN
Sbjct: 241 QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMDMRKLFNPPLKGYGN 300

Query: 301 FVGTVCAMDNVKDLLSGSLLRVVRIKKAKVSLNEHFTSTIVTPRSGSDESINYENIVGF 360
          FVGTVCAMDNVKDLLSGSLLRVVRIKKAKVSLNEHFTSTIVTP SGSDESINYENIVGF
Sbjct: 301 FVGTVCAMDNVKDLLSGSLLRVVRIKKAKVSLNEHFTSTIVTPCSGSDESINYENIVGF 360

Query: 361 GDRRRRLGFDEVD FGWGHADNVSLVQHGLKDVS VVQSYFLFIRPPKNNPDG IKILSFMPPS 420
          GDRRRRLGFDEVD FGWGHADNVSLVQHGLKDVS VVQSYFLFIRPPKNNPDG IKILSFMPP
Sbjct: 361 GDRRRRLGFDEVD FGWGHADNVSLVQHGLKDVS VVQSYFLFIRPPKNNPDG IKILSFMPP 420

Query: 421 IVKSFKFEMETMTNKYVTKP 440
          I+KSFKFEMETMTNKYVTKP
  
```

Sbjct: 421 IMKSFKFEMETMTNKYVTKP 440

CPU time: 0.08 user secs. 0.03 sys. secs 0.11 total secs.

Lambda	K	H
0.321	0.139	0.414

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1809

Number of Sequences: 0

Number of extensions: 119

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 440

length of database: 414,047,803

effective HSP length: 129

effective length of query: 311

effective length of database: 414,047,674

effective search space: 128768826614

effective search space used: 128768826614

T: 9

A: 40

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 76 (33.9 bits)